OncoPro Panel基因检测报告

**OncoPro Panel Gene Testing Report**

## 1. 检测总览 Testing Overview

## 1.1项目简介 Introduction

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| 检测方法Testing method：基于杂交捕获的高通量测序法（Hybridization Capture-based NGS） |
| 检测平台Testing platform：Nextseq CN500 |
| 检测内容Testing purpose：通过OncoPro Panel基因进行测序，测定患者肿瘤组织中*BRAF*基因的状态。Detect the BRAF mutation(s) in the patient tumor tissue specimen by OncoPro NGS panel. |

## 1.2 送检信息

|  |  |  |  |
| --- | --- | --- | --- |
| 受检者信息 subject info | | | |
| 研究中心Site Name: | {{sample.site\_name}} | **中心编号**Site ID: | {{sample.site\_ID}} |
| 受试者编号Subject ID: | {{sample.subject\_ID}} | **性 别**Gender: | {%if sample.gender==”男”%}☑男Male □女Female{%elif sample.gender==”女”%}□男Male ☑女Female {%else%}□男Male □女Female {%endif%} |
| 疾病类型Disease Type： | {{sample.primary\_disease}} | **出生年份**Year of Birth: | {{sample.birthday}} |
| 取材部位anatomic location： | {{sample.anatomic\_site}} |  |  |

|  |  |  |  |
| --- | --- | --- | --- |
| 受检样本信息 sample info | | | |
| 样本编码Sample ID: | {{sample.specimen\_parent\_id}} | **样本类型**Specimen Type: | {{sample.sample\_type}} |
| 样本数量Specimen amount: | {{sample.tissue\_specimen\_amount}} | **采集日期**Specimen Collection Date: | {{sample.tissue\_collection\_date}} |
| 切片日期Sectioning Date: | {{sample.section\_date}} | **接收日期**Reception Date: | {{sample.tissue\_date\_received}} |
| 报告日期Report Date: | {{sample.report\_date}} |  |  |

## 1.3 检测结果 Testing Results

* **BRAF Class I/II/III检测结果 BRAF Class I/II/III NGS Results**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **基因名称**  **Gene** | **类型**  **Type** | **基因变异分类**  **Genetic Alteration** | **检出位点**  **Mutation Detected** | **检测结果**  **Result detected (Yes/No)** |
| *BRAF*  *Class I* | SNV | V600E/K/D/R/M/G/A/L | {%tr if var.SNV\_I%} | |
| {%tr for a in var.SNV\_I%} | |
| *{{a.hgvs\_p|replace(“p.”, “”)}}* | *检出*  *Yes* |
| {%tr endfor%} | |
| {%tr else%} | |
| *未检出*  *No* | *未检出*  *No* |
| {%tr endif%} | |
| *BRAF*  *Class II* | SNV | Q257R,K499E,P367L/S,L505H/F,I463S,L525R,G464V/E/R/A,E586K,G469A/V/R,L597Q/R/S/V,V471F,T599I/K/R,L485W/F,K601E/N/T/Q | {%tr if var.SNV\_II%} | |
| {%tr for a in var.SNV\_II%} | |
| *{{a.hgvs\_p|replace(“p.”, “”)}}* | *检出*  *Yes* |
| {%tr endfor%} | |
| {%tr else%} | |
| *未检出*  *No* | *未检出*  *No* |
| {%tr endif%} | |
| Short Indel | N486\_A489delinsK  N486\_P490del (∆NVTAP)  V487\_P492delinsA  T488\_P492del (∆TAPTP)  P490\_Q494del (∆PTPQQ)  T599TT/TS  V600\_K601delinsE  K601\_S602delinsNT | {%tr if var.Indel%} | |
| {%tr for a in var.Indel%} | |
| *{{a.hgvs\_p|replace(“p.”, “”)}}* | *检出*  *Yes* |
| {%tr endfor%} | |
| {%tr else%} | |
| *未检出*  *No* | *未检出*  *No* |
| {%tr endif%} | |
| Fusion | Fusions that retain intact BRAF kinase domain with breakpoints that typically occur within introns 7-10 (exons 8-11 in RNA) | {%tr if var.Fusion%} | |
| {%tr for a in var.Fusion%} | |
| *{{a.gene\_symbol}}* | *检出*  *Yes* |
| {%tr endfor%} | |
| {%tr else%} | |
| *未检出*  *No* | *未检出*  *No* |
| {%tr endif%} | |
| Splice Variant | Removing multiple exons upstream of the kinase domain | {%tr if var.Splice%} | |
| {%tr for a in var.Splice%} | |
| *{{a.hgvs\_c|replace(“c.”, “”)}}* | *检出*  *Yes* |
| {%tr endfor%} | |
| {%tr else%} | |
| *未检出*  *No* | *未检出*  *No* |
| {%tr endif%} | |
| *BRAF*  *Class III* | SNV | F247L,Q524L,D287H,R558Q,V459L,N581I/S/T/Y,G466A/E/V/R,D594A/G/H/N/V/E/Y,S467L,F595L,G469E,G596D/R,K483E,T599A | {%tr if var.SNV\_III%} | |
| {%tr for a in var.SNV\_III%} | |
| *{{a.hgvs\_p|replace(“p.”, “”)}}* | *检出*  *Yes* |
| {%tr endfor%} | |
| {%tr else%} | |
| *未检出*  *No* | *未检出*  *No* |
| {%tr endif%} | |

**Detail results：SNV/Short Indel/Splice Variant**

**{%p if var.SNV\_I+var.SNV\_II+var.SNV\_III+var.Indel+var.Splice%}**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **变异类型**  **Variation type** | **基因名称**  **Gene** | **转录本**  **Transcript ID** | **外显子/内含子**  **Exon/Intron** | **碱基变化**  **NT Change** | **氨基酸变化**  **AA Change** | **突变丰度**  **Alteration Frequency**  **（VAF）** |
| {%tr for a in var.SNV\_I+var.SNV\_II+var.SNV\_III+var.Indel+var.Splice%} | | | | | | |
| SNV | *BRAF* | {{a.transcript\_primary}} | {{a.gene\_region}} | {{a.hgvs\_c}} | {{a.hgvs\_p}} | {{a.freq\_str}} |
| {%tr endfor%} | | | | | | |

{%p esle%}

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **变异类型**  **Variation type** | **基因名称**  **Gene** | **转录本**  **Transcript ID** | **外显子/内含子**  **Exon/Intron** | **碱基变化**  **NT Change** | **氨基酸变化**  **AA Change** | **突变丰度**  **Alteration Frequency**  **（VAF）** |
| SNV | *BRAF* | - | - | - | - | - |

{%p endif%}

**Detail results：Fusion**

**{%p if var.Fusion%}**

|  |  |  |
| --- | --- | --- |
| **变异类型**  **Variation type** | **基因名称Gene** | **融合模式Fusion Type** |
| {%tr for a in var.Fusion%} | | |
| Fusion | *BRAF* | {{a.var\_id}} |
| {%tr endfor%} | | |

{%p else%}

|  |  |  |
| --- | --- | --- |
| **变异类型**  **Variation type** | **基因名称Gene** | **融合模式Fusion Type** |
| Fusion | *BRAF* | - |

{%p endif%}

* **检测方法 Testing Method**

样本核酸提取后采用“人类100基因突变联合检测试剂盒（高通量测序法）”（厦门艾德生物医药科技股份有限公司）进行文库构建和目标区域捕获，测序平台为贝瑞和康Nextseq CN500。组织样本分析软件为XXXX。

After the sample nucleic acid extraction, the library construction and target region capture are carried out by the AmoyDx® OncoPro Panel (High Throughput Sequencing), the sequencing platform is berrygenomics NextSeq CN500. The analysis software for tissue sample is XXXX

|  |  |  |
| --- | --- | --- |
| **试剂盒名称**  **Key Reagent** | **货号**  **Cat.No.** | **批号**  **Lot.No.** |
| 人类100基因突变联合检测试剂盒（高通量测序法）  AmoyDx® OncoPro Panel (High Throughput Sequencing) | 待定 TBD | 待定 TBD |

**2. 数据质控结果**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **质控内容**  **QC parameter** | | **合格标准**  **QC Criteria** | **质控结果**  **QC Result** | **是否合格**  **Pass/Fail** |
| 病理质控  Pathology QC |  |  |  |  |
| 提取质控Extraction QC |  |  |  |  |
| 文库质控  Library QC |  |  |  |  |
| 数据质控  Output QC |  |  |  |  |

检测人 operator： 复核人 reviewer： 审批人 approver：

注：本报告仅针对本次送检样本，该检测为肿瘤患者个体化治疗提供依据，仅供科研参考。